



Sequence Listing 60117-39.txt

SEQUENCE LISTING

<110> Winkler, David
Latham, John
Skonier, John
Shpektor, Diana
Hayes, Trenton
Geoghegan, James

<120> Ligands for TGF-Beta Binding Proteins and Uses Thereof

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<140> US10/799,162

<141> 2004-03-12

<150> PCT/US2004/007565

<151> 2004-03-12

<150> 60/455,253

<151> 2003-03-14

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<212> DNA

<213> Homo sapiens

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 35           40           45
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 50           55           60
Pro Pro His His Pro Phe Glu Thr Lys Asp Val Ser Glu Tyr Ser Cys
 65           70           75           80
Arg Glu Leu His Phe Thr Arg Tyr Val Thr Asp Gly Pro Cys Arg Ser
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130           135           140
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Ser Glu Leu Lys Asp Phe Gly Thr Glu Ala Ala Arg Pro Gln Lys Gly
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<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

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<210> 8

<211> 213

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<213> Homo sapiens

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Ala Thr Glu Ile Ile Arg Glu Leu Gly Glu Tyr Pro Glu Pro Pro Pro
 35             40             45
Glu Leu Glu Asn Asn Lys Thr Met Asn Arg Ala Glu Asn Gly Gly Arg
 50             55             60
Pro Pro His His Pro Phe Glu Thr Lys Asp Val Ser Glu Tyr Ser Cys
 65             70             75             80
Arg Glu Leu His Phe Thr Arg Tyr Val Thr Asp Gly Pro Cys Arg Ser
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Ser Glu Leu Lys Asp Phe Gly Thr Glu Ala Ala Arg Pro Gln Lys Gly
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195            200            205
Leu Glu Asn Ala Tyr
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<212> DNA

<213> Cercopithecus pygerythrus

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<212> PRT

<213> Cercopithecus pygerythrus

Sequence Listing 60117-39.txt

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 20           25           30
Ala Thr Glu Ile Ile Pro Glu Leu Gly Glu Tyr Pro Glu Pro Pro Pro
 35           40           45
Glu Leu Glu Asn Asn Lys Thr Met Asn Arg Ala Glu Asn Gly Gly Arg
 50           55           60
Pro Pro His His Pro Phe Glu Thr Lys Asp Val Ser Glu Tyr Ser Cys
 65           70           75           80
Arg Glu Leu His Phe Thr Arg Tyr Val Thr Asp Gly Pro Cys Arg Ser
 85           90           95
Ala Lys Pro Val Thr Glu Leu Val Cys Ser Gly Gln Cys Gly Pro Ala
100           105           110
Arg Leu Leu Pro Asn Ala Ile Gly Arg Gly Lys Trp Trp Arg Pro Ser
115           120           125
Gly Pro Asp Phe Arg Cys Ile Pro Asp Arg Tyr Arg Ala Gln Arg Val
130           135           140
Gln Leu Leu Cys Pro Gly Gly Ala Ala Pro Arg Ala Arg Lys Val Arg
145           150           155           160
Leu Val Ala Ser Cys Lys Cys Lys Arg Leu Thr Arg Phe His Asn Gln
165           170           175
Ser Glu Leu Lys Asp Phe Gly Pro Glu Ala Ala Arg Pro Gln Lys Gly
180           185           190
Arg Lys Pro Arg Pro Arg Ala Arg Gly Ala Lys Ala Asn Gln Ala Glu
195           200           205
Leu Glu Asn Ala Tyr
210

```

<210> 11

<211> 638

<212> DNA

<213> Mus musculus

<400> 11

```

atgcagccct cactagcccc gtgcctcatc tgcctacttg tgcacgctgc cttctgtgct 60
gtggagggcc aggggtggca agccttcagg aatgatgcca cagaggctcat cccagggctt 120
ggagagtacc ccgagcctcc tcctgagaac aaccagacca tgaaccgggc ggagaatgga 180
ggcagacctc ccacccatcc ctatgacgcc aaaggtgtgt ccgagtacag ctgccgcgag 240
ctgcactaca cccgcttcct gacagacggc ccatgccgca gcgccaagcc ggtcaccgag 300
ttggtgtgct ccggccagtg cggccccgcg cggtgtgctgc ccaacgccat cgggcgcgtg 360
aagtgggtggc gcccgaaagg accggatttc cgctgcatcc cggatcgcta ccgcgcgcag 420
cgggtgcagc tgctgtgccc cgggggcgcg gcgcgcgcgt cgcgcaaggt gcgtctggtg 480
gcctcgtgca agtgcaagcg cctcaccgcg ttccacaacc agtcggagct caaggacttc 540
gggccggaga ccgcgcggcc gcagaagggt cgcaagccgc ggcccggcgc ccggggagcc 600
aaagccaacc aggcggagct ggagaacgcc tactagag 638

```

<210> 12

<211> 211

<212> PRT

<213> Mus musculus

<400> 12

```

Met Gln Pro Ser Leu Ala Pro Cys Leu Ile Cys Leu Leu Val His Ala
 1           5           10           15
Ala Phe Cys Ala Val Glu Gly Gln Gly Trp Gln Ala Phe Arg Asn Asp
 20           25           30

```

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```

Ala Thr Glu Val Ile Pro Gly Leu Gly Glu Tyr Pro Glu Pro Pro Pro
   35           40           45
Glu Asn Asn Gln Thr Met Asn Arg Ala Glu Asn Gly Gly Arg Pro Pro
   50           55           60
His His Pro Tyr Asp Ala Lys Asp Val Ser Glu Tyr Ser Cys Arg Glu
   65           70           75           80
Leu His Tyr Thr Arg Phe Leu Thr Asp Gly Pro Cys Arg Ser Ala Lys
           85           90           95
Pro Val Thr Glu Leu Val Cys Ser Gly Gln Cys Gly Pro Ala Arg Leu
           100          105          110
Leu Pro Asn Ala Ile Gly Arg Val Lys Trp Trp Arg Pro Asn Gly Pro
           115          120          125
Asp Phe Arg Cys Ile Pro Asp Arg Tyr Arg Ala Gln Arg Val Gln Leu
           130          135          140
Leu Cys Pro Gly Gly Ala Ala Pro Arg Ser Arg Lys Val Arg Leu Val
           145          150          155          160
Ala Ser Cys Lys Cys Lys Arg Leu Thr Arg Phe His Asn Gln Ser Glu
           165          170          175
Leu Lys Asp Phe Gly Pro Glu Thr Ala Arg Pro Gln Lys Gly Arg Lys
           180          185          190
Pro Arg Pro Gly Ala Arg Gly Ala Lys Ala Asn Gln Ala Glu Leu Glu
           195          200          205
Asn Ala Tyr
           210

```

<210> 13
 <211> 674
 <212> DNA
 <213> Rattus norvegicus

```

<400> 13
gaggaccgag tgccttcct cttcttgga ccatgcagct ctactagcc cttgccttg 60
cctgcctgct tgtacatgca gccttcgttg ctgtggagag ccaggggtgg caagccttca 120
agaatgatgc cacagaaatc atcccgggac tcagagagta cccagagcct cctcaggaac 180
tagagaacaa ccagaccatg aaccgggagg agaacggagg cagaccccc caccatcctt 240
atgacaccaa agacgtgtcc gagtacagct gccgcgagct gcactacacc cgcttcgtga 300
ccgacggccc gtgccgcagt gccaaagccg tcaccgagtt ggtgtgctcg ggccagtgcg 360
gccccgcgcg gctgctgccc aacgccatcg ggcgcgtgaa gtggtggcgc ccgaacggac 420
ccgacttcgg ctgcatcccg gatcgctacc gcgcgcagcg ggtgcagctg ctgtgccccg 480
gcggcgcggc gccgcgctcg cgcaaggtgc gtctggtggc ctcgtgcaag tgcaagcgcc 540
tcacccgctt ccacaaccag tcggagctca agacttcgg acctgagacc gcgcggccgc 600
agaagggtcg caagccgcgg cccgcgccc ggggagccaa agccaaccag gcggagctgg 660
agaacgccta ctag                                     674

```

<210> 14
 <211> 213
 <212> PRT
 <213> Rattus norvegicus

```

<400> 14
Met Gln Leu Ser Leu Ala Pro Cys Leu Ala Cys Leu Leu Val His Ala
   1           5           10          15
Ala Phe Val Ala Val Glu Ser Gln Gly Trp Gln Ala Phe Lys Asn Asp
           20          25          30
Ala Thr Glu Ile Ile Pro Gly Leu Arg Glu Tyr Pro Glu Pro Pro Gln
           35          40          45
Glu Leu Glu Asn Asn Gln Thr Met Asn Arg Ala Glu Asn Gly Gly Arg
           50          55          60

```


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```

Pro Pro His His Pro Tyr Asp Thr Lys Asp Val Ser Glu Tyr Ser Cys
65      70      75      80
Arg Glu Leu His Tyr Thr Arg Phe Val Thr Asp Gly Pro Cys Arg Ser
      85      90      95
Ala Lys Pro Val Thr Glu Leu Val Cys Ser Gly Gln Cys Gly Pro Ala
      100      105      110
Arg Leu Leu Pro Asn Ala Ile Gly Arg Val Lys Trp Trp Arg Pro Asn
      115      120      125
Gly Pro Asp Phe Arg Cys Ile Pro Asp Arg Tyr Arg Ala Gln Arg Val
      130      135      140
Gln Leu Leu Cys Pro Gly Gly Ala Ala Pro Arg Ser Arg Lys Val Arg
      145      150      155      160
Leu Val Ala Ser Cys Lys Cys Lys Arg Leu Thr Arg Phe His Asn Gln
      165      170      175
Ser Glu Leu Lys Asp Phe Gly Pro Glu Thr Ala Arg Pro Gln Lys Gly
      180      185      190
Arg Lys Pro Arg Pro Arg Ala Arg Gly Ala Lys Ala Asn Gln Ala Glu
      195      200      205
Leu Glu Asn Ala Tyr
      210

```

<210> 15
 <211> 532
 <212> DNA
 <213> Bos torus

```

<400> 15
agaatgatgc cacagaaatc atccccgagc tgggcgagta ccccgagcct ctgccagagc 60
tgaacaacaa gaccatgaac cgggcggaga acggagggag acctcccccac caccctttg 120
agaccaaaga cgcctccgag tacagctgcc gggagctgca cttcaccgcg tacgtgaccg 180
atgggcccgtg ccgcagcgcc aagccgggtca ccgagctggg gtgctcgggc cagtgcggcc 240
cggcgcgccct gctgcccac gccatcggcc gcggcaagtg gtggcgccca agcgggccc 300
acttcgctg catccccgac cgctaccgcg cgcagcgggt gcagctgttg tgtcctggcg 360
gcgcggcgcc gcgcgcgcgc aaggtgcgcc tgggtggcctc gtgcaagtgc aagcgccctca 420
ctcgcctcca caaccagtcc gagctcaagg acttcggggc cgaggccgcg cggccgcaaa 480
cgggcccggaa gctgcggccc cgcgcccggg gcaccaaagc cagccgggccc ga 532

```

<210> 16
 <211> 176
 <212> PRT
 <213> Bos torus

```

<400> 16
Asn Asp Ala Thr Glu Ile Ile Pro Glu Leu Gly Glu Tyr Pro Glu Pro
1      5      10      15
Leu Pro Glu Leu Asn Asn Lys Thr Met Asn Arg Ala Glu Asn Gly Gly
      20      25      30
Arg Pro Pro His His Pro Phe Glu Thr Lys Asp Ala Ser Glu Tyr Ser
      35      40      45
Cys Arg Glu Leu His Phe Thr Arg Tyr Val Thr Asp Gly Pro Cys Arg
      50      55      60
Ser Ala Lys Pro Val Thr Glu Leu Val Cys Ser Gly Gln Cys Gly Pro
      65      70      75      80
Ala Arg Leu Leu Pro Asn Ala Ile Gly Arg Gly Lys Trp Trp Arg Pro
      85      90      95
Ser Gly Pro Asp Phe Arg Cys Ile Pro Asp Arg Tyr Arg Ala Gln Arg
      100      105      110
Val Gln Leu Leu Cys Pro Gly Gly Ala Ala Pro Arg Ala Arg Lys Val

```

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115	120	125														
Arg	Leu	Val	Ala	Ser	Cys	Lys	Cys	Lys	Arg	Leu	Thr	Arg	Phe	His	Asn	
130						135					140					
Gln	Ser	Glu	Leu	Lys	Asp	Phe	Gly	Pro	Glu	Ala	Ala	Arg	Pro	Gln	Thr	
145					150					155					160	
Gly	Arg	Lys	Leu	Arg	Pro	Arg	Ala	Arg	Gly	Thr	Lys	Ala	Ser	Arg	Ala	
				165					170						175	

<210> 17
 <211> 232
 <212> PRT
 <213> Homo sapiens

<400> 17																
Met	Glu	Arg	Cys	Pro	Ser	Leu	Gly	Val	Thr	Leu	Tyr	Ala	Leu	Val	Val	
1			5					10					15			
Val	Leu	Gly	Leu	Arg	Ala	Thr	Pro	Ala	Gly	Gly	Gln	His	Tyr	Leu	His	
			20				25					30				
Ile	Arg	Pro	Ala	Pro	Ser	Asp	Asn	Leu	Pro	Leu	Val	Asp	Leu	Ile	Glu	
		35				40					45					
His	Pro	Asp	Pro	Ile	Phe	Asp	Pro	Lys	Glu	Lys	Asp	Leu	Asn	Glu	Thr	
	50					55					60					
Leu	Leu	Arg	Ser	Leu	Leu	Gly	Gly	His	Tyr	Asp	Pro	Gly	Phe	Met	Ala	
65				70					75					80		
Thr	Ser	Pro	Pro	Glu	Asp	Arg	Pro	Gly	Gly	Gly	Gly	Gly	Ala	Ala	Gly	
				85				90					95			
Gly	Ala	Glu	Asp	Leu	Ala	Glu	Leu	Asp	Gln	Leu	Leu	Arg	Gln	Arg	Pro	
			100				105					110				
Ser	Gly	Ala	Met	Pro	Ser	Glu	Ile	Lys	Gly	Leu	Glu	Phe	Ser	Glu	Gly	
		115					120					125				
Leu	Ala	Gln	Gly	Lys	Lys	Gln	Arg	Leu	Ser	Lys	Lys	Leu	Arg	Arg	Lys	
		130				135					140					
Leu	Gln	Met	Trp	Leu	Trp	Ser	Gln	Thr	Phe	Cys	Pro	Val	Leu	Tyr	Ala	
145				150					155					160		
Trp	Asn	Asp	Leu	Gly	Ser	Arg	Phe	Trp	Pro	Arg	Tyr	Val	Lys	Val	Gly	
			165					170					175			
Ser	Cys	Phe	Ser	Lys	Arg	Ser	Cys	Ser	Val	Pro	Glu	Gly	Met	Val	Cys	
		180					185					190				
Lys	Pro	Ser	Lys	Ser	Val	His	Leu	Thr	Val	Leu	Arg	Trp	Arg	Cys	Gln	
		195				200						205				
Arg	Arg	Gly	Gly	Gln	Arg	Cys	Gly	Trp	Ile	Pro	Ile	Gln	Tyr	Pro	Ile	
	210				215					220						
Ile	Ser	Glu	Cys	Lys	Cys	Ser	Cys									
225					230											

<210> 18
 <211> 420
 <212> DNA
 <213> Homo sapiens

<400> 18																
gagctccggc	gggtcagccg	gactgtcggc	ttcccggggc	atctgggtcc	ggcggggcac	60										
agccctgggc	gctgccgaag	ccgccgccgc	cgcctccgcg	gcgagtacag	gcggttccc	120										
ccggagcctg	tgcagctcca	gctcctcggg	ggtggagaag	tggggggtgg	gggtgatgta	180										
tggggggaag	aagggggagg	ggccaacccc	gagagagtca	gtggtttcca	tggtgatgga	240										
gctgaaagtg	caggaaattt	aaaggcttgg	accctgcgag	acagacaaac	cggtgccaac	300										
gtgcgcggac	gccgccgccg	ccgccgccgc	tggagtccgc	cgggcagagc	cggccgcgga	360										

Sequence Listing 60117-39.txt

gcccggagca ggcggaggga agtgccccta gaaccagctc agccagcggc gcttgacacag 420

<210> 19
<211> 218
<212> PRT
<213> Homo sapiens

<400> 19
Met Pro Ser Leu Pro Ala Pro Pro Ala Pro Leu Leu Leu Leu Gly Leu
1 5 10 15
Leu Leu Leu Gly Ser Arg Pro Ala Arg Gly Ala Gly Pro Glu Pro Pro
20 25 30
Val Leu Pro Ile Arg Ser Glu Lys Glu Pro Leu Pro Val Arg Gly Ala
35 40 45
Ala Gly Cys Thr Phe Gly Gly Lys Val Tyr Ala Leu Asp Glu Thr Trp
50 55 60
His Pro Asp Leu Gly Glu Pro Phe Gly Val Met Arg Cys Val Leu Cys
65 70 75 80
Ala Cys Glu Ala Pro Gln Trp Gly Arg Arg Thr Arg Gly Pro Gly Arg
85 90 95
Val Ser Cys Lys Asn Ile Lys Pro Glu Cys Pro Thr Pro Ala Cys Gly
100 105 110
Gln Pro Arg Gln Leu Pro Gly His Cys Cys Gln Thr Cys Pro Gln Glu
115 120 125
Arg Ser Ser Ser Glu Arg Gln Pro Ser Gly Leu Ser Phe Glu Tyr Pro
130 135 140
Arg Asp Pro Glu His Arg Ser Tyr Ser Asp Arg Gly Glu Pro Gly Ala
145 150 155 160
Glu Glu Arg Ala Arg Gly Asp Gly His Thr Asp Phe Val Ala Leu Leu
165 170 175
Thr Gly Pro Arg Ser Gln Ala Val Ala Arg Ala Arg Val Ser Leu Leu
180 185 190
Arg Ser Ser Leu Arg Phe Ser Ile Ser Tyr Arg Arg Leu Asp Arg Pro
195 200 205
Thr Arg Ile Arg Phe Ser Asp Ser Asn Gly
210 215

<210> 20
<211> 420
<212> DNA
<213> Homo sapiens

<400> 20
cccgggtcag cgcccgcccg cccgcgctcc tcccggccgc tcctcccgcg ccgcccggcc 60
cggcgcgcgac tctgcggccg ccgacgagc ccctcgccgc actgccccgg ccccggcccc 120
ggccccggcc ccctcccgcg gcaccgcccc cggccccggc ctccgcccct cgcactcccg 180
cctccctccc tccgcccgt cccgcgccct cctccctccc tcctcccag ctgtcccggt 240
cgcgctcatgc cgagcctccc ggccccgcg gccccgctgc tgctcctcgg gctgctgctg 300
ctcggtctccc ggccggcccg cggcgccggc cccgagcccc ccgtgctgcc catccgttct 360
gagaaggagc cgctgcccgt tcggggagcg gcaggctgca ccttcggcgg gaaggtctat 420